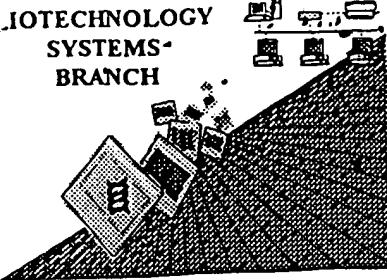


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/963761

Source: OIPE

Date Processed by STIC: 10/10/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/963761</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPIIA" HEADERS, WHICH WERE INSERTED BY PTO		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID.NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Entered: ① Input 33; Found 25
 ② Sequences are misordered/misnumbered

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001
TIME: 14:20:54

Input Set : A:\ES.txt
Output Set: N:\CRF3\10102001\I963761.raw

SEQUENCE LISTING

2 (1) GENERAL INFORMATION:

3 (i) APPLICANT: TZahi ARAZI, YOEL MOSHE SHIBOLETH
4 AND AMIT GAL-ON

5 (ii) TITLE OF INVENTION: VECTORS FOR EXPRESSING HETEROLOGOUS
6 PEPTIDES
7 AT THE AMINO-TERMINUS OF POTYVIRUS COAT
8 Protein, methods for use thereof, plants infected with

same and methods of

W--> 9

vaccination using same ✓

11 (iii) NUMBER OF SEQUENCES: 33

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Mark M. Friedman C/O Mr. Bill Polkinghorn
15 Discovery Dispatch

16 (B) STREET: 9003 Florin Way

17 (C) CITY: Upper Marlboro

18 (D) STATE: Maryland

19 (E) COUNTRY: United States of America

20 (F) ZIP: 20772

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

23 (B) COMPUTER: Twinhead* Slimnote-890TX

24 (C) OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11

25 (D) SOFTWARE: Word for Windows version 2.0 converted to
an ASCII file

Does Not Comply
Corrected Diskette Needed

① Input 33; Found 25
② Sequences are misordered/
misnumbered

28 (vi) CURRENT APPLICATION DATA:

29 (A) APPLICATION NUMBER: US/09/963,761 ✓

C--> 30 (B) FILING DATE: 27-Sep-2001

31 (C) CLASSIFICATION: XXX

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 60/253,136

34 (B) FILING DATE: 28 November, 2000

C--> 35 (A) APPLICATION NUMBER:

C--> 36 (B) FILING DATE:

C--> 37 (A) APPLICATION NUMBER: ✓

C--> 38 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Friedmam, Mark M.

41 (B) REGISTRATION NUMBER: 33,883

42 (C) REFERENCE/DOCKET NUMBER: 1686/4

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 972-3-5625553

45 (B) TELEFAX: 972-3-5625554

46 (C) TELEX:

Entered

*Input 33 Found 25
Sequences misnumbered*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001
TIME: 14:20:54

Input Set : A:\ES.txt
Output Set: N:\CRF3\10102001\I963761.raw

ERRORED SEQUENCES

121 (2) INFORMATION FOR SEQ ID NO: 3:
 122 (i) SEQUENCE CHARACTERISTICS:
 123 (A) LENGTH: 20
 124 (B) TYPE: nucleic acid
 125 (C) STRANDEDNESS: Single
 126 (D) TOPOLOGY: linear
 127 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 130 CATTTCCTTT CACGGCGTGGC 20
E--> 132 (2) INFORMATION FOR SEQ ID NO:4:
 132 (2) INFORMATION FOR SEQ ID NO: 4:
 133 (i) SEQUENCE CHARACTERISTICS:
 134 (A) LENGTH: 21
 135 (B) TYPE: nucleic acid
 136 (C) STRANDEDNESS: Single
 137 (D) TOPOLOGY: linear
 138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 140 TCACACCAC ACCATCACCA T
E--> 142 (2) INFORMATION FOR SEQ ID NO:5:
 153 (2) INFORMATION FOR SEQ ID NO: 6:
 154 (i) SEQUENCE CHARACTERISTICS:
 155 (A) LENGTH: 53
 156 (B) TYPE: nucleic acid
 157 (C) STRANDEDNESS: Single
 158 (D) TOPOLOGY: linear
 159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 161 CAGCTGCAGT CACACCAC CAATCACCAT TCAGGCACTC AGCCAACTGT 50
 162 GGC
E--> 165 (2) INFORMATION FOR SEQ ID NO:7:
 165 (2) INFORMATION FOR SEQ ID NO: 7:
 166 (i) SEQUENCE CHARACTERISTICS:
 167 (A) LENGTH: 55
 168 (B) TYPE: nucleic acid
 169 (C) STRANDEDNESS: Single
 170 (D) TOPOLOGY: linear
 171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 173 CAGCTGCAGT CACACCAC CAATCACCAT GATACTGGAG CTACAAAGAA 50
 174 AGAAG
E--> 176 (2) INFORMATION FOR SEQ ID NO:8:
 176 (2) INFORMATION FOR SEQ ID NO: 8:
 177 (i) SEQUENCE CHARACTERISTICS:
 178 (A) LENGTH: 55
 179 (B) TYPE: nucleic acid
 180 (C) STRANDEDNESS: Single
 181 (D) TOPOLOGY: linear
 182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 184 TCAGCATCAG AGCAGAAGCT CATTTCAGAG GAGGATCTCG GATCC 45
E--> 186 (2) INFORMATION FOR SEQ ID NO:9:
 186 (2) INFORMATION FOR SEQ ID NO: 9:

(21) sequences w/o numbered

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

(55)

Erroneous Input 55
Found 95

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001
TIME: 14:20:54

Input Set : A:\ES.txt
Output Set: N:\CRF3\10102001\I963761.raw

187 (i) SEQUENCE CHARACTERISTICS:
 188 (A) LENGTH: 15
 189 (B) TYPE: amino acid
 190 (C) STRANDEDNESS: single
 191 (D) TOPOLOGY: linear
 192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 193 Ser Ala Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gly Ser
 E--> 194 5 10
 196 (2) INFORMATION FOR SEQ ID NO:10:
 196 (2) INFORMATION FOR SEQ ID NO: 10:
 197 (i) SEQUENCE CHARACTERISTICS:
 198 (A) LENGTH: 77
 199 (B) TYPE: nucleic acid
 200 (C) STRANDEDNESS: Single
 201 (D) TOPOLOGY: linear
 202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 204 CAGCTGCAGT CAGCATCAGA GCAGAAGCTC ATTTAGAGG AGGATCTCGG 50
 205 ATCCCTAGGC ACTCAGCAA CTGTGGC 77
 E--> 208 (2) INFORMATION FOR SEQ ID NO:11:
 208 (2) INFORMATION FOR SEQ ID NO: 11:
 209 (i) SEQUENCE CHARACTERISTICS:
 210 (A) LENGTH: 82
 211 (B) TYPE: nucleic acid
 212 (C) STRANDEDNESS: Single
 213 (D) TOPOLOGY: linear
 E--> 214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:
 216 CAGCTGCAGT CAGCATCAGA GCAGAAGCTC ATTTAGAGG AGGATCTCGG 50
 217 ATCCGATACT GGAGCTACAA AGAAAGATAA AG 82
 E--> 219 (2) INFORMATION FOR SEQ ID NO:12:
 219 (2) INFORMATION FOR SEQ ID NO: 12:
 220 (i) SEQUENCE CHARACTERISTICS:
 221 (A) LENGTH: 81
 222 (B) TYPE: nucleic acid
 223 (C) STRANDEDNESS: Single
 224 (D) TOPOLOGY: linear
 225 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 227 CAGCTGCAGT CAGCATCAGA GCAGAAGCTC ATTTAGAGG AGGATCTCGG 50
 228 ATCCAAGAAA GATAAAGAAG ATGACAAAGG G 81
 E--> 230 (2) INFORMATION FOR SEQ ID NO:13:
 230 (2) INFORMATION FOR SEQ ID NO: 13:
 231 (i) SEQUENCE CHARACTERISTICS:
 232 (A) LENGTH: 81
 233 (B) TYPE: nucleic acid
 234 (C) STRANDEDNESS: Single
 235 (D) TOPOLOGY: linear
 E--> 236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:
 238 CGCGGATCCG ATGACAAAGG GAAAAACAAG G 81
 E--> 241 (2) INFORMATION FOR SEQ ID NO:14:
 241 (2) INFORMATION FOR SEQ ID NO: 14:

Input 15
Found 14
15

Sequence
not ordered

Sequence
not ordered

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001
TIME: 14:20:54

Input Set : A:\ES.txt
Output Set: N:\CRF3\10102001\I963761.raw

242 (i) SEQUENCE CHARACTERISTICS:
 243 (A) LENGTH: 30
 244 (B) TYPE: nucleic acid
 245 (C) STRANDEDNESS: Single
 246 (D) TOPOLOGY: linear
 247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 249 CTCGGATCCA ACAAGGATGT TACAGGCTCC
 E--> 251 (2) INFORMATION FOR SEQ ID NO:15: (30)
 251 (2) INFORMATION FOR SEQ ID NO: 15: — sequence not ordered
 252 (i) SEQUENCE CHARACTERISTICS:
 253 (A) LENGTH: 27
 254 (B) TYPE: nucleic acid
 255 (C) STRANDEDNESS: Single
 256 (D) TOPOLOGY: linear
 257 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 259 CGCGGATCCG GCTCCGGCTC AAGTGAG (27)
 E--> 261 (2) INFORMATION FOR SEQ ID NO:16:
 261 (2) INFORMATION FOR SEQ ID NO: 16:
 262 (i) SEQUENCE CHARACTERISTICS:
 263 (A) LENGTH: 30
 264 (B) TYPE: nucleic acid
 265 (C) STRANDEDNESS: Single
 266 (D) TOPOLOGY: linear
 267 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 269 CGCGGATCCG AGAAAACAGT GGCAGCTGTC (30)
 E--> 271 (2) INFORMATION FOR SEQ ID NO:17:
 271 (2) INFORMATION FOR SEQ ID NO: 17:
 272 (i) SEQUENCE CHARACTERISTICS:
 273 (A) LENGTH: 28
 274 (B) TYPE: nucleic acid
 275 (C) STRANDEDNESS: Single
 276 (D) TOPOLOGY: linear
 277 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 279 CGCGGATCCG CTGTCACGAA GGACAAGG (28)
 E--> 281 (2) INFORMATION FOR SEQ ID NO:18:
 281 (2) INFORMATION FOR SEQ ID NO: 18:
 282 (i) SEQUENCE CHARACTERISTICS:
 283 (A) LENGTH: 33
 284 (B) TYPE: nucleic acid
 285 (C) STRANDEDNESS: Single
 286 (D) TOPOLOGY: linear
 287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 289 CGCGGATCCA AGGATGTAAA TGCTGGTTCT CAT (33)
 E--> 291 (2) INFORMATION FOR SEQ ID NO:19:
 291 (2) INFORMATION FOR SEQ ID NO: 19:
 292 (i) SEQUENCE CHARACTERISTICS:
 293 (A) LENGTH: 30
 294 (B) TYPE: nucleic acid
 295 (C) STRANDEDNESS: Single

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001
TIME: 14:20:54

Input Set : A:\ES.txt
Output Set: N:\CRF3\10102001\I963761.raw

296 (D) TOPOLOGY: linear
 297 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 299 CTCGGATCCG GTTCTCATGG GAAAATTGTG
E--> 301 (2) INFORMATION FOR SEQ ID NO: 20: 30
 301 (2) INFORMATION FOR SEQ ID NO: 20: sequence mis ordered
 302 (i) SEQUENCE CHARACTERISTICS:
 303 (A) LENGTH: 51
 304 (B) TYPE: nucleic acid
 305 (C) STRANDEDNESS: Single
 306 (D) TOPOLOGY: linear
 307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 309 AGTGTGAGAG GAGATCTTCA AGTGCTTGCA CGAAAAGCAG CAAGACCACT 50
 310 T 51
E--> 312 (2) INFORMATION FOR SEQ ID NO: 21:
 312 (2) INFORMATION FOR SEQ ID NO: 21:
 313 (i) SEQUENCE CHARACTERISTICS:
 314 (A) LENGTH: 17
 315 (B) TYPE: amino acid
 316 (C) STRANDEDNESS: single
 317 (D) TOPOLOGY: linear
 318 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
 320 Ser Val Arg Gly Asp Leu Gln Val Leu Ala Arg Lys Ala Ala Arg
E--> 321 5 10 15
 322 Pro Leu
 323 17
 325 (2) INFORMATION FOR SEQ ID NO: 22:
 325 (2) INFORMATION FOR SEQ ID NO: 22:
 326 (i) SEQUENCE CHARACTERISTICS:
 327 (A) LENGTH: 87
 328 (B) TYPE: nucleic acid
 329 (C) STRANDEDNESS: Single
 330 (D) TOPOLOGY: linear
 331 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 333 CAGCTGCAGT CCGTGAGAGG AGATCTTCAA GTGCTTGAC GAAAAGCAGC 50
 334 AAGACCACTT AAGAAAGATA AAAAGATGA CAAAGGG 87
E--> 336 (2) INFORMATION FOR SEQ ID NO: 23:
 336 (2) INFORMATION FOR SEQ ID NO: 23:
 337 (i) SEQUENCE CHARACTERISTICS:
 338 (A) LENGTH: 83
 339 (B) TYPE: nucleic acid
 340 (C) STRANDEDNESS: Single
 341 (D) TOPOLOGY: linear
 342 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 344 CAGCTGCAGA GTGTGAGAGG AGATCTTCAA GTGCTTGAC GAAAAGCAGC 50
 345 AAGACCACTT TCAGGCACTC AGCCAAGTGT GGC 83
E--> 348 (2) INFORMATION FOR SEQ ID NO: 24:
 348 (2) INFORMATION FOR SEQ ID NO: 24:
 349 (i) SEQUENCE CHARACTERISTICS:
 350 (A) LENGTH: 84

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001
TIME: 14:20:54

Input Set : A:\ES.txt
Output Set: N:\CRF3\10102001\I963761.raw

```

351      (B) TYPE: nucleic acid
352      (C) STRANDEDNESS: Single
353      (D) TOPOLOGY: linear
354      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
356 CGCGGATCCG TGAGAGGAGA TCTTCAAGTG CTTGCACGAA AAGCAGCAAG 50
357 ACCACTTAAG AAAGATAAAAG AAGATGACAA AGGG               84
E--> 359 (2) INFORMATION FOR SEQ ID NO:25:
359 (2) INFORMATION FOR SEQ ID NO: 25:
360   (i) SEQUENCE CHARACTERISTICS:
361     (A) LENGTH: 33
362     (B) TYPE: nucleic acid
363     (C) STRANDEDNESS: Single
364     (D) TOPOLOGY: linear
365     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
367 CAGCTGCAGT CCGAGAAAAAC AGTGGCAGCT GTC
E--> 369 (2) INFORMATION FOR SEQ ID NO:26?
399 (2) INFORMATION FOR SEQ ID NO: 29:
400   (i) SEQUENCE CHARACTERISTICS:
401     (A) LENGTH: 8
402     (B) TYPE: amino acid
403     (C) STRANDEDNESS: single
404     (D) TOPOLOGY: linear
405     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:
407 Ser Ile Ile Asn Phe Glu Lys Leu
E--> 408
410 (2) INFORMATION FOR SEQ ID NO:30:

```

33
sequencer misnumbered

5
misaligned amino numbering
expected as read at
end of file Identifier
8

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001
TIME: 14:20:55

Input Set : A:\ES.txt
Output Set: N:\CRF3\10102001\I963761.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:9 M:259 W: Allowed number of lines exceeded, (ii) TITLE OF INVENTION:
L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:38 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:132 M:254 E: No. of Bases conflict, Input:0 Counted:30 SEQ:3
L:132 M:320 E: (1) Wrong Nucleic Acid Designator, 17
L:132 M:204 E: No. of Bases differ, LENGTH:Input:20 Counted:45 SEQ:3
L:142 M:254 E: No. of Bases conflict, Input:0 Counted:31 SEQ:4
L:142 M:320 E: (1) Wrong Nucleic Acid Designator, 17
L:142 M:204 E: No. of Bases differ, LENGTH:Input:21 Counted:46 SEQ:4
L:165 M:254 E: No. of Bases conflict, Input:0 Counted:63 SEQ:6
L:165 M:320 E: (1) Wrong Nucleic Acid Designator, 17
L:165 M:204 E: No. of Bases differ, LENGTH:Input:53 Counted:78 SEQ:6
L:176 M:254 E: No. of Bases conflict, Input:0 Counted:65 SEQ:7
L:176 M:320 E: (1) Wrong Nucleic Acid Designator, 17
L:176 M:204 E: No. of Bases differ, LENGTH:Input:55 Counted:80 SEQ:7
L:186 M:254 E: No. of Bases conflict, Input:0 Counted:55 SEQ:8
L:186 M:320 E: (1) Wrong Nucleic Acid Designator, 17
L:186 M:204 E: No. of Bases differ, LENGTH:Input:55 Counted:70 SEQ:8
L:194 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:208 M:254 E: No. of Bases conflict, Input:0 Counted:87 SEQ:10
L:208 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:208 M:204 E: No. of Bases differ, LENGTH:Input:77 Counted:102 SEQ:10
L:214 M:202 E: (16) Value must be an Integer, Data=[x:]
L:219 M:254 E: No. of Bases conflict, Input:0 Counted:92 SEQ:11
L:219 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:219 M:204 E: No. of Bases differ, LENGTH:Input:82 Counted:107 SEQ:11
L:230 M:254 E: No. of Bases conflict, Input:0 Counted:91 SEQ:12
L:230 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:230 M:204 E: No. of Bases differ, LENGTH:Input:81 Counted:106 SEQ:12
L:236 M:202 E: (16) Value must be an Integer, Data=[x:]
L:241 M:254 E: No. of Bases conflict, Input:0 Counted:41 SEQ:13
L:241 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:241 M:204 E: No. of Bases differ, LENGTH:Input:31 Counted:56 SEQ:13
L:251 M:254 E: No. of Bases conflict, Input:0 Counted:40 SEQ:14
L:251 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:251 M:204 E: No. of Bases differ, LENGTH:Input:30 Counted:55 SEQ:14
L:261 M:254 E: No. of Bases conflict, Input:0 Counted:37 SEQ:15
L:261 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:261 M:204 E: No. of Bases differ, LENGTH:Input:27 Counted:52 SEQ:15
L:271 M:254 E: No. of Bases conflict, Input:0 Counted:40 SEQ:16
L:271 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:271 M:204 E: No. of Bases differ, LENGTH:Input:30 Counted:55 SEQ:16
L:281 M:254 E: No. of Bases conflict, Input:0 Counted:38 SEQ:17
L:281 M:320 E: (1) Wrong Nucleic Acid Designator, 18

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/963,761

DATE: 10/10/2001

TIME: 14:20:55

Input Set : A:\ES.txt

Output Set: N:\CRF3\10102001\I963761.raw

L:281 M:204 E: No. of Bases differ, LENGTH:Input:28 Counted:53 SEQ:17
L:291 M:254 E: No. of Bases conflict, Input:0 Counted:43 SEQ:18
L:291 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:291 M:204 E: No. of Bases differ, LENGTH:Input:33 Counted:58 SEQ:18
L:301 M:254 E: No. of Bases conflict, Input:0 Counted:40 SEQ:19
L:301 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:301 M:204 E: No. of Bases differ, LENGTH:Input:30 Counted:55 SEQ:19
L:312 M:254 E: No. of Bases conflict, Input:0 Counted:61 SEQ:20
L:312 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:312 M:204 E: No. of Bases differ, LENGTH:Input:51 Counted:76 SEQ:20
L:321 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
L:336 M:254 E: No. of Bases conflict, Input:0 Counted:97 SEQ:22
L:336 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:336 M:204 E: No. of Bases differ, LENGTH:Input:87 Counted:112 SEQ:22
L:348 M:254 E: No. of Bases conflict, Input:0 Counted:93 SEQ:23
L:348 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:348 M:204 E: No. of Bases differ, LENGTH:Input:83 Counted:108 SEQ:23
L:359 M:254 E: No. of Bases conflict, Input:0 Counted:94 SEQ:24
L:359 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:359 M:204 E: No. of Bases differ, LENGTH:Input:84 Counted:109 SEQ:24
L:369 M:254 E: No. of Bases conflict, Input:0 Counted:43 SEQ:25
L:369 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:369 M:204 E: No. of Bases differ, LENGTH:Input:33 Counted:58 SEQ:25
L:379 M:254 E: No. of Bases conflict, Input:0 Counted:44 SEQ:26
L:379 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:379 M:204 E: No. of Bases differ, LENGTH:Input:34 Counted:59 SEQ:26
L:389 M:254 E: No. of Bases conflict, Input:0 Counted:47 SEQ:27
L:389 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:389 M:204 E: No. of Bases differ, LENGTH:Input:37 Counted:62 SEQ:27
L:399 M:254 E: No. of Bases conflict, Input:0 Counted:34 SEQ:28
L:399 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:399 M:204 E: No. of Bases differ, LENGTH:Input:24 Counted:49 SEQ:28
L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
L:421 M:254 E: No. of Bases conflict, Input:0 Counted:66 SEQ:30
L:421 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:421 M:204 E: No. of Bases differ, LENGTH:Input:56 Counted:81 SEQ:30
L:433 M:254 E: No. of Bases conflict, Input:0 Counted:43 SEQ:31
L:433 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:433 M:204 E: No. of Bases differ, LENGTH:Input:56 Counted:58 SEQ:31
L:444 M:254 E: No. of Bases conflict, Input:0 Counted:32 SEQ:32
L:444 M:320 E: (1) Wrong Nucleic Acid Designator, 18
L:444 M:204 E: No. of Bases differ, LENGTH:Input:22 Counted:47 SEQ:32